



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.

(ii) TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
(B) STREET: 6 Becker Farm Road
(C) CITY: Roseland
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/467,265
(B) FILING DATE: 06-JUN-1995
(C) CLASSIFICATION:

a' (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ferraro, Gregory D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-456

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 31..843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGGGAACGT GTTTCTCCCC TCGTTTGGTC ATG GAG GCG CTG CCC CTG CTA GCC																54	
Met Glu Ala Leu Pro Leu Leu Ala																	
1 5																	
GCG	ACA	ACT	CCG	GAC	CAC	GGC	CGC	CAC	CGA	AGG	CTG	CTT	CTG	CTG	CCG	102	
Ala	Thr	Thr	Pro	Asp	His	Gly	Arg	His	Arg	Arg	Leu	Leu	Leu	Leu	Pro		
10						15						20					
CTA	CTG	CTG	TTC	CTG	CTG	CCG	GCT	GGA	GCT	GTG	CAG	GGC	TGG	GAG	ACA	150	
Leu	Leu	Leu	Phe	Leu	Leu	Pro	Ala	Gly	Ala	Val	Gln	Gly	Trp	Glu	Thr		
25					30						35			40			
GAG	GAG	AGG	CCC	CGG	ACT	CGC	GAA	GAG	GAG	TGC	CAC	TTC	TAC	GCG	GGT	198	
Glu	Glu	Arg	Pro	Arg	Thr	Arg	Glu	Glu	Glu	Cys	His	Phe	Tyr	Ala	Gly		
			45						50						55		
GGA	CAA	GTG	TAC	CCG	GGA	GAG	GCA	TCC	CGG	GTA	TGC	GTC	GCC	GAC	CAC	246	
Gly	Gln	Val	Tyr	Pro	Gly	Glu	Ala	Ser	Arg	Val	Ser	Val	Ala	Asp	His		
			60						65						70		
TCC	CTG	CAC	CTA	AGC	AAA	GCG	AAG	ATT	TCC	AAG	CCA	GCG	CCC	TAC	TGG	294	
Ser	Leu	His	Leu	Ser	Lys	Ala	Lys	Ile	Ser	Lys	Pro	Ala	Pro	Tyr	Trp		
75						80						85					
GAA	GGA	ACA	GCT	GTG	ATC	GAT	GGA	GAA	TTT	AAG	GAG	CTG	AAG	TTA	ACT	342	
Glu	Gly	Thr	Ala	Val	Ile	Asp	Gly	Glu	Phe	Lys	Glu	Leu	Lys	Leu	Thr		
90						95						100					
GAT	TAT	CGT	GGG	AAA	TAC	TTG	GTT	TTC	TTC	TTC	TAC	CCA	CTT	GAT	TTC	390	
Asp	Tyr	Arg	Gly	Lys	Tyr	Leu	Val	Phe	Phe	Phe	Tyr	Pro	Leu	Asp	Phe		
105					110						115			120			
ACA	TTT	GTG	TGT	CCA	ACT	GAA	ATT	ATC	GCT	TTT	GGC	GAC	AGA	CTT	GAA	438	
Thr	Phe	Val	Cys	Pro	Thr	Glu	Ile	Ile	Ala	Phe	Gly	Asp	Arg	Leu	Glu		
			125						130						135		
GAA	TTC	AGA	TCT	ATA	AAT	ACT	GAA	GTG	GTA	GCA	TGC	TCT	GTT	GAT	TCA	486	
Glu	Phe	Arg	Ser	Ile	Asn	Thr	Glu	Val	Val	Ala	Cys	Ser	Val	Asp	Ser		
			140						145						150		
CAG	TTT	ACC	CAT	TTG	GCC	TGG	ATT	AAT	ACC	CCT	CGA	AGA	CAA	GGA	GGA	534	
Gln	Phe	Thr	His	Leu	Ala	Trp	Ile	Asn	Thr	Pro	Arg	Arg	Gln	Gly	Gly		
155						160						165					
CTT	GGG	CCA	ATA	AGG	ATT	CCA	CTT	CTT	TCA	GAT	TTG	ACC	CAT	CAG	ATC	582	
Leu	Gly	Pro	Ile	Arg	Ile	Pro	Leu	Leu	Ser	Asp	Leu	Thr	His	Gln	Ile		
170						175						180					
TCA	AAG	GAC	TAT	GGT	GTA	TAC	CTA	GAG	GAC	TCA	GGC	CAC	ACT	CTT	AGA	630	
Ser	Lys	Asp	Tyr	Gly	Val	Tyr	Leu	Glu	Asp	Ser	Gly	His	Thr	Leu	Arg		
185						190						195			200		
GGT	CTC	TTC	ATT	ATT	GAT	GAC	AAA	GGA	ATC	CTA	AGA	CAA	ATT	ACT	CTG	678	
Gly	Leu	Phe	Ile	Ile	Asp	Asp	Lys	Gly	Ile	Leu	Arg	Gln	Ile	Thr	Leu		
			205						210						215		

AAT GAT CTT CCT GTG GGT AGA TCA GTG GAT GAG ACA CTA CGT TTG GTT	726
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val	
220 225 230	
CAA GCA TTC CAG TAC ACT GAC AAA CAC GGA GAA GTC TGC CCT GCT GGC	774
Gln Ala Phe Gln Tyr Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly	
235 240 245	
TGG AAA CCT GGT AGT GAA ACA ATA ATC CCA GAT CCA GCT GGA AAG CTG	822
Trp Lys Pro Gly Ser Glu Thr Ile Ile Pro Asp Pro Ala Gly Lys Leu	
250 255 260	
AAG TAT TTC GAT AAA CTG AAT TGAGAAATAC TTCTTCAAGT TATGATGCTT	873
Lys Tyr Phe Asp Lys Leu Asn	
265 270	
GAAAGTTCTC AATAAAGTTC ACGGTTTCAT TACCACAAAA AAAAA	918

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg	
1 5 10 15	
His Arg Arg Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala	
20 25 30	
Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu	
35 40 45	
Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala	
50 55 60	
Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys	
65 70 75 80	
Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly	
85 90 95	
Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val	
100 105 110	
Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile	
115 120 125	
Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu	
130 135 140	
Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile	
145 150 155 160	

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

29

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

23

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCCATGGC TGGAGCTGTG CAGGG

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGTCTAGA TCAATTCAGT TTATCGAAAT ACTTCAGC

38

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGGATCC GCTGGAGCTG TGCAGG

26

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGATCCC GAGGCGCTGC CCCTGC

26

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCT CAATTCAGTT TATCGAAATA C

31

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA GCGCTGCCC CTG

33

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGATCCT CAATTCAGTT TATCGAAATC A

31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGCGGATCC ACCATGGAGG CGCTG

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGCTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA ATTCAGTTTA TC

52

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys

1		5		10		15									
Ala	Thr	Ala	Val	Met	Pro	Asp	Gly	Gln	Phe	Lys	Asp	Ile	Ser	Leu	Ser
		20					25						30		
Asp	Tyr	Lys	Gly	Lys	Tyr	Val	Val	Phe	Phe	Phe	Tyr	Pro	Leu	Asp	Phe
	35					40						45			
Thr	Phe	Val	Cys	Pro	Thr	Glu	Ile	Ile	Ala	Phe	Ser	Asp	Arg	Ala	Glu
	50					55					60				
Glu	Phe	Lys	Lys	Leu	Asn	Cys	Gln	Val	Ile	Gly	Ala	Ser	Val	Asp	Ser
65				70						75				80	
His	Phe	Cys	His	Leu	Ala	Trp	Val	Asn	Thr	Pro	Lys	Lys	Gln	Gly	Gly
			85					90					95		
Leu	Gly	Pro	Met	Asn	Ile	Pro	Leu	Val	Ser	Asp	Pro	Lys	Arg	Thr	Ile
		100						105					110		
Ala	Gln	Asp	Tyr	Gly	Val	Leu	Lys	Ala	Asp	Glu	Gly	Ile	Ser	Phe	Arg
	115						120					125			
Gly	Leu	Phe	Ile	Ile	Asp	Asp	Lys	Gly	Ile	Leu	Arg	Gln	Ile	Thr	Val
	130					135					140				
Asn	Asp	Pro	Pro	Cys	Cys	Arg	Ser	Val	Asp	Glu	Thr	Leu	Arg	Leu	Val
145				150						155				160	
Gln	Ala	Phe	Gln	Phe	Thr	Asp	Lys	His	Gly	Glu	Val	Cys	Pro	Ala	Gly
			165						170					175	
Trp	Lys	Pro	Gly	Ser	Asp	Thr	Ile	Lys	Pro	Asp	Val	Pro	Lys	Thr	Lys
		180						185					190		
Glu	Tyr	Phe	Ser	Lys	Gln	Lys									
	195														

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Ala	Ser	Gly	Asn	Ala	Arg	Ile	Gly	Lys	Pro	Ala	Pro	Asp	Phe	Lys
1				5				10						15	
Ala	Thr	Ala	Val	Val	Asp	Gly	Ala	Phe	Lys	Glu	Val	Lys	Leu	Ser	Asp
	20						25						30		

Tyr Lys Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr
 35 40 45
 Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asn Arg Ala Glu Asp
 50 55 60
 Phe Arg Lys Leu Gly Cys Glu Val Leu Gly Val Ser Val Asp Ser Gln
 65 70 75 80
 Phe Asn His Leu Ala Trp Ile Asn Thr Pro Arg Lys Glu Gly Gly Leu
 85 90 95
 Gly Pro Leu Asn Ile Pro Leu Leu Gly Asp Val Thr Arg Arg Leu Ser
 100 105 110
 Glu Asp Tyr Gly Val Leu Lys Thr Asp Glu Gly Ile Ala Tyr Arg Gly
 115 120 125
 Leu Phe Ile Ile Asp Gly Lys Gly Val Leu Arg Gln Ile Thr Val Asn
 130 135 140
 Asp Leu Pro Val Gly Arg Ser Val Asp Glu Ala Leu Arg Leu Val Gln
 145 150 155 160
 Ala Phe Gln Tyr Thr Asp Glu His Gly Glu Val Cys Pro Ala Gly Trp
 165 170 175
 Lys Pro Gly Ser Asp Thr Ile Lys Pro Asn Val Asp Asp Ser Lys Glu
 180 185 190
 Tyr Phe Ser Lys His Asn
 195

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Ala Ala Ala Gly Arg Leu Leu Trp Ser Ser Val Ala Arg Gly
 1 5 10 15
 Ala Ser Ala Ile Ser Arg Ser Ile Ser Ala Ser Thr Val Leu Arg Pro
 20 25 30
 Val Ala Ser Arg Arg Thr Cys Leu Thr Asp Ile Leu Trp Ser Ala Ser
 35 40 45
 Ala Gln Gly Lys Ser Ala Phe Ser Thr Ser Ser Ser Phe His Thr Pro
 50 55 60

Ala	Val	Thr	Gln	His	Ala	Pro	Tyr	Phe	Lys	Gly	Thr	Ala	Val	Val	Asn
65					70					75					80
Gly	Glu	Phe	Lys	Glu	Leu	Ser	Leu	Asp	Asp	Phe	Lys	Gly	Lys	Tyr	Leu
			85						90					95	
Val	Leu	Phe	Phe	Tyr	Pro	Leu	Asp	Phe	Thr	Phe	Val	Cys	Pro	Thr	Glu
			100					105					110		
Ile	Val	Ala	Phe	Ser	Asp	Lys	Ala	Asn	Glu	Phe	His	Asp	Val	Asn	Cys
		115					120					125			
Glu	Val	Val	Ala	Val	Ser	Val	Asp	Ser	His	Phe	Ser	His	Leu	Ala	Trp
		130				135					140				
Ile	Asn	Thr	Pro	Arg	Lys	Asn	Gly	Gly	Leu	Gly	His	Met	Asn	Ile	Thr
145					150					155					160
Leu	Leu	Ser	Asp	Ile	Thr	Lys	Gln	Ile	Ser	Arg	Asp	Tyr	Gly	Val	Leu
				165					170					175	
Leu	Glu	Ser	Ala	Gly	Ile	Ala	Leu	Arg	Gly	Leu	Phe	Ile	Ile	Asp	Pro
			180					185					190		
Asn	Gly	Val	Val	Lys	His	Leu	Ser	Val	Asn	Asp	Leu	Pro	Val	Gly	Arg
		195					200					205			
Ser	Val	Glu	Glu	Thr	Leu	Arg	Leu	Val	Lys	Ala	Phe	Gln	Phe	Val	Glu
		210				215					220				
Thr	His	Gly	Glu	Val	Cys	Pro	Ala	Asn	Trp	Thr	Pro	Glu	Ser	Pro	Thr
225					230					235					240
Ile	Lys	Pro	Ser	Pro	Thr	Ala	Ser	Lys	Glu	Tyr	Phe	Glu	Lys	Val	His
				245					250					255	

Gln

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ser	Ser	Gly	Asn	Ala	Lys	Ile	Gly	Tyr	Pro	Ala	Pro	Asn	Phe	Lys
1				5				10						15	
Ala	Thr	Ala	Val	Met	Pro	Asp	Gly	Gln	Phe	Lys	Asp	Ile	Ser	Leu	Ser

20					25					30						
Glu	Tyr	Lys	Gly	Lys	Tyr	Val	Val	Phe	Phe	Phe	Tyr	Pro	Leu	Asp	Phe	
35					40					45						
Thr	Phe	Val	Cys	Pro	Thr	Glu	Ile	Ile	Ala	Phe	Ser	Asp	Arg	Ala	Asp	
50					55					60						
Glu	Phe	Lys	Lys	Leu	Asn	Cys	Gln	Val	Ile	Gly	Ala	Ser	Val	Asp	Ser	
65					70					75					80	
His	Phe	Cys	His	Leu	Ala	Trp	Ile	Asn	Thr	Pro	Lys	Lys	Gln	Gly	Gly	
85					90					95						
Leu	Gly	Pro	Met	Asn	Ile	Pro	Leu	Ile	Ser	Asp	Pro	Lys	Arg	Thr	Ile	
100					105					110						
Ala	Gln	Asp	Tyr	Gly	Val	Leu	Lys	Ala	Asp	Glu	Gly	Ile	Ser	Phe	Arg	
115					120					125						
Gly	Leu	Phe	Ile	Ile	Asp	Asp	Lys	Gly	Ile	Leu	Arg	Gln	Ile	Thr	Ile	
130					135					140						
Asn	Asp	Leu	Pro	Val	Gly	Arg	Ser	Val	Asp	Glu	Ile	Ile	Arg	Leu	Val	
145					150					155					160	
Gln	Ala	Phe	Gln	Phe	Thr	Asp	Lys	His	Gly	Glu	Val	Cys	Pro	Ala	Gly	
165					170					175						
Trp	Lys	Pro	Gly	Ser	Asp	Thr	Ile	Lys	Pro	Asp	Val	Asn	Lys	Ser	Lys	
180					185					190						
Glu	Tyr	Phe	Ser	Lys	Gln	Lys										
195																

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